

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Portugal, Frank H.  
Colwell, Rita R.  
Hug, Anwarul  
Chowdhury, Afzal

(ii) TITLE OF INVENTION: Compositions and Methods for  
Differentiating Among *Shigella* Species  
and *Shigella* from *E. coli* Species

(iii) NUMBER OF SEQUENCES: 22

### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.  
(B) STREET: 816 Congress Avenue, Suite 1900  
(C) CITY: Austin  
(D) STATE: Texas  
(E) COUNTRY: USA  
(F) ZIP: 78701

### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not Yet Assigned  
(B) FILING DATE: Concurrently Herewith  
(C) CLASSIFICATION: Not Yet Assigned

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,117  
(B) FILING DATE: 20-FEB-1997

### (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Norberg, Gloria L.  
(B) REGISTRATION NUMBER: 36,706  
(C) REFERENCE/DOCKET NUMBER: 044198.0000

### (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 499-6200  
(B) TELEFAX: (512) 499-6290

## (2) INFORMATION FOR SEQ ID NO:1:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAGTTTGAT CATGGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTTACCT TGTTACGACT T 21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCAGGC CTAACACATG CAAGTCGAAC 60  
GGTAACAGGA AGCAGCTTGC TGTTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG 120  
GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG 180  
CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG 240  
CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC 300  
CAGCCACACT GGAAGTGA CACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGGAATAT 360  
TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCGCGTGT ATGAAGAAGG CCTTCGGGTT 420  
GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTTGCTC ATTGACGTTA 480  
CCCGCAGAAG AAGCACCAGC TAACTCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA 540  
GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA 600  
AATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG 660  
GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAAAGAT CTGGAGGAAT ACCGGTGGCG 720  
AAGGCGGCCC CTTGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGGA GCAAACAGGA 780  
TTAGATACCC TGGTAGTCCA CGCTGTAAAC GATGTCGACT TGGAGGTTGT GCCCTTGAGG 840  
TGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA 900  
AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTGCATGC 960  
AACGCGAAGA ACCTTACCTG GTCTTGACAT CCACGGAAGT TTTCAGAGAT GAGAATGTGC 1020  
CTTCGGGAAC CGTGAGACAG GTGCTGCATG GCTGTCGTCA GCTCGTGTG TGAAATGTTG 1080  
GGTTAAGTCC CGCAACGAGC GCAACCCTTA TCCTTTGTTG CCAGCGGTCC GGCCGGGAAC 1140  
TCAAAGGAGA CTGCCAGTGA TAACTGGAG GAAGGTGGGG ATGACGTCAA GTCATCATGG 1200  
CCCTTACGAC CAGGGCTACA CACGTGCTAC AATGGCGCAT ACAAAGAGAA GCGACCTCGC 1260

GAGAGCAAGC GGACCTCATA AAGTGCGTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC 1320  
 CATGAAGTCG GAATCGCTAG TAATCGTGGA TCAGAATGCC ACGGTGAATA CGTTCCTGGG 1380  
 5 CCTTGATACAC ACCGCCCCGTC ACACCATGGG AGTGGGTTGC AAAAGAAGTA GGTAGCTTAA 1440  
 CCTTCGGGAG GGCCTTACC ACTTTGTGAT TCATGACTGG GGTGAAGTCG TAACAAGGTA 1500  
 10 ACCGTA 1506

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCAGGC CTAACACATG CAAGTCGAAC 60  
 GGTAACAGGA AACAGCTTGC TGTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG 120  
 25 GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG 180  
 CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG 240  
 30 CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC 300  
 CAGCCACACT GGAAGTGA GACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGGAATAT 360  
 TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCGCGTGT ATGAAGAAGG CCTTCGGGTT 420  
 35 GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTTACTC ATTGACGTTA 480  
 CCCGCAGAAG AAGCACCGGC TAACTCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA 540  
 40 GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA 600  
 AATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG 660  
 GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAGAGAT CTGGAGGAAT ACCGGTGGCG 720  
 45 AAGGCGGCCC CCTGGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGGA GCAAACAGGA 780  
 TTAGATACCC TGGTAGTCCA CGCCGTAAAC GATGTCGACT TGGAGGTTGT GCCCTTGAGG 840  
 50 CGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA 900  
 AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTCGACGC 960  
 55 AACGCGAAGA ACTTACCTGG TCCTGACATC CACGGAACCT TCCAGAGATG GATTGGTGCC 1020  
 TTCGGGAAC TGTGAGACAG TGCTGCATGG CTGTCGTCAG CTCGTGTTGT GAAATGTTGG 1080  
 GTTAAGTCCC GCAACGAGCG CAACCTTAT CTTTTGTTGC CAGCGGTCCG GCCGGGAAC 1140  
 60 CAAAGGAGAC TGCCAGTGAT AACTGGAGG AAGGTGGGGA TGACGTCAAG TCATCATGGC 1200  
 CCTTACGACC AGGGCTACAC ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG 1260  
 65 AGAGCAAGCG GACCTCATAA AGTGCGTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320

	ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGCCA CGGTGAATAC GTTCCCGGGC	1380
	CTTGTAACACA CCGCCCGTCA CACCATGGGA GTGGGTTGCA AAAGAAGTAG GTAGCTTAAC	1440
5	CTTCGGGAGG GCGCTTACCA CTTTGTGATT CATGACTGGG GTGAAGTCGT AACAAGGTAA	1500
	CCGTA	1505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: one-of(400, 593, 642, 737, 968, 998)
- (D) OTHER INFORMATION: /mod\_base= OTHER

/note= "N = Unknown"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGCGCAGGC CTAACACATG CAAGTCGAAC	60
GGTAACAGAA AGCAGCTTGC TCCTTTGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG	120
GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG	180
CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG	240
CTAGTAGTGG GGTAACGGCT CACCTAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC	300
AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT GGGGAATATT	360
GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTN TGAANAAGGC CTTCCGGGTTG	420
TAAAGTACTT TCAGCGGGGA GGAAGGGAGT AAAGTTAATA CCTTTGCTCA TTGACGTTAC	480
CCGCAGAAGA AGCACCGGCT AACTCCGTGC CAGCAGCCGC GGTAATACCG AGGGTGCAAG	540
CGTTAATCGG AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAAT CANATGTGAA	600
ATCCCCGGGC TCAACCTGGG AACTGCATCT GATACTGGCA ANCTTGAGTC TCGTAGAGGG	660
GGGTAGAAAT CCAGGTGTAG CGGTGAAATG CGTAGAGATC TGGAGGAATA CCGGTGGCGA	720
AGGCGGCCCC CTGGACNAAG ACTGACGCTC AGGTGCGAAA GCGTGGGGAG CAAACAGGAT	780
TAGATACCCT GGTAGTCCAC GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC	840
GTGGCTTCCG GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA	900
ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA ATTCGATGCA	960
ACGCGAANAA CCTTACCTGG TCTTGACATC CACAGAANCT TCCAGAGATG GATTGGTGCC	1020
TTCCGGGAAT GTGAGACAGG TGCTGCATGG CTGTCGTCAG CTCGTGTTGT GAAATGTTGG	1080
GTTAAGTCCC GCAACGAGCG CAACCCCTAT CCTTTGTTGC CAGCGGTCCG GCCGGGAAT	1140
CAAAGGAGAC TGCCAGTGAT AAAGTGGAGG AAGGTGGGGA TGACGTCAAG TCATCATGGC	1200

CCTTACGACC AGGGCTACAC ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG 1260  
 AGAGCAAGCG GACCTCATAA AGTGCGTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320  
 5 ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGTCA CGGTGAATAC GTTCCCGGGC 1380  
 CTTGTACACA CCGCCCGTCA CACCATGGGA GTGGCTTAAC CTTCCGGGAGG GCGCTTACCA 1440  
 10 CTTTGTGATT CAT 1453

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCGAGGC CTAACACATG CAAGTCGAAC 60  
 GGTAACAGGA AGCAGCTTGC TCTTCGCTGA CGAGTGGCGG ACGGGTGAGT AATGTCTGGG 120  
 25 AAAGTGCCTG ATGGAGGGGG ATAATACTG GAAACGGTAG CTAATACCGC ATAATGTCCG 180  
 AAGACCAAAG AGGGGGACCT TCGGGCCTCT TGCCATCGGA TGTGCCCAGA TGGGATTAGC 240  
 30 TTGTTGGTGG GGTAACGGCT CACCAAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC 300  
 AGCCACATGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTG GGAATATTG 360  
 CACAATGGGC GCAAGCCTGA TGCAGCCATG CCGCGTGTAT GAAGAAGGCC TTCGGGTTGT 420  
 35 AAAGTACTTT CAGCGGGGAG GAAGGGAGTA AAGTTAATAC CTTTGCTCAT TGACGTTACC 480  
 CGCAGAAGAA GCACCGGCTA ACTCCGTGCC AGCAGCCGCG GTAATACGGA GGGTGCAAGC 540  
 40 GTTAATCGGA ATTACTGGGC GTAAAGCGCA CGCAGGCGGT TTGTTAAGTC AGATGTGAAA 600  
 TCCCCGGGCT CAACCTGGGA ACTGCATCTG ATACTGGCAA GCTTGAGTCT CGTAGAGGGG 660  
 45 GGTAGAATTC CAGGTGTAGC GGTGAAATGC GTAGAGATCT GGAGGAATAC CCGTGGCGAA 720  
 GGCGGCCCCC TGGACGAAGA CTGACGCTCA GGTGCGAAAG CGTGGGGAGC AAACAGGATT 780  
 AGATACCCTG GTAGTCCACG CCGTAAACGA TGTCGACTTG GAGGTTGTGC CCTTGAGGCG 840  
 50 TGGCTTCCGG AGCTAACGCG TTAAGTCGAC CGCCTGGGGA GTACGGCCGC AAGGTTAAAA 900  
 CTCAAATGAA TTGACGGGGG CCCGCACAAG CCGTGGAGCA TGTGGTTTAA TTCGATGCAA 960  
 CGCGAAGAAC CTTACCTGGT CTTGACATCC ACGGAAGTTT TCAGAGATGA GAATGTGCCT 1020  
 55 TCGGGAACCG TGAGACAGGT GCTGCATGGC TGTCGTCAGC TCGTGTGTG AAATGTTGGG 1080  
 TTAAGTCCCG CAACGAGCGC AACCTTATC CTTTGTGTC AGCGGTCCGG CCGGGAACCTC 1140  
 60 AAAGGAGACT GCCAGTGATA AACTGGAGGA AGGTGGGGAT GACGTCAAGT CATCATGGCC 1200  
 CTTACGACCA GGGCTACACA CGTGCTACAA TGGCGCATAC AAAGAGAAGC GACCTCGCGA 1260  
 65 GAGCAAGCGG ACCTCATAAA GTGCGTCCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320

	ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGCCA CGGTGAATAC GTTCCCGGGC	1380
	CTTGACACACA CCGCCCGTCA CACCATGGGA GTGGGTTGCA AAAGAAGTAG GTAGCTTAAC	1440
5	CTTCGGGAGG GCGCTTACCA CTTTGTGATT CATGACTGGG GTGAAGTCGT AACAAGGTAA	1500
	CCGTA	1505

10 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20	AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA	60
	GTGCAACGGT AACAGGAAGA AGCTTGCTCT TTGCTGACGA GTGGCGGACG GGTGAGTAAT	120
	GTCTGGGAAA CTGCCTGATG GAGGGGGATA ACTACTGGAA ACGGTAGCTA ATACCGCATA	180
25	ACGTCGCAAG ACCAAAGAGG GGGACCTTCG GGCCTCTTGC CATCGGATGT GCCCAGATGG	240
	GATTAGCTAG TAGGTGGGGT AACGGCTCAC CTAGGCGACG ATCCCTAGCT GGTCTGAGAG	300
30	GATGACCAGC CACACTGGAA CTGAGACACG GTCCAGACTC CTACGGGAGG CAGCAGTGGG	360
	GAATATTGCA CAATGGGCGC AAGCCTGATG CAGCCATGCC GCGTGTATGA AGAAGGCCTT	420
	CGGGTTGTAA AGTACTTTCA GCGGGGAGGA AGGGAGTAAA GTTAATACCT TTGCTCATTG	480
35	ACGTTACCCG CAGAAGAAGC ACCGGCTAAC TCCGTGCCAG CAGCCGCGGT AATACGGAGG	540
	GTGCAAGCGT TAATCGGAAT TACTGGGCGT AAAGCGCACG CAGGCGGTTT GTTAAGTCAG	600
40	ATGTGAAATC CCCGGGCTCA ACCTGGGAAC TGCATCTGAT ACTGGCAAGC TTGAGTCTCG	660
	TAGAGGGGGG TAGAATTCCA GGTGTAGCGG TGAAATGCGT AGAGATCTGG AGGAATACCG	720
	GTGGCGAAGG CGGCCCCCTG GACGAAGACT GACGCTCAGG TGCAGAAAGC TGGGGAGCAA	780
45	ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG TCGACTTGGA GGTGTGCCCC	840
	TTGAGGCGTG GCTTCCGGAG CTAACGCGTT AAGTCGACCG CCTGGGGAGT ACGGCCGCAA	900
50	GGTTAAAAC TCAAATGAATT GACGGGGGCC CGCACAAAGC GTGGAGCATG TGGTTTAATT	960
	CGATGCAACG CGAAGAACCT TACCTGGTCT TGACATCCAC GGAAGTTTTC AGAGATGAGA	1020
	ATGTGCCTTC GGAACCGTG AGACAGGTGC TGCATGGCTG TCGTCAGCTC GTGTTGTGAA	1080
55	ATGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTATCCT TTGTTGCCAG CCGTCCGGCC	1140
	GGGAAC TCAA AGGAGACTGC CAGTGATAAA CTGGAGGAAG GTGGGGATGA CGTCAAGTCA	1200
60	TCATGGCCCT TACGACCAGG GCTACACACG TGCTACAATG GCGCATACAA AGAGAAGCGA	1260
	CCTCGCGAGA GCAAGCGGAC CTCATAAAGT GCGTCGTAGT CCGGATTGGA GTCTGCAACT	1320
65	CGACTCCATG AAGTCGGAAT CGCTAGTAAT CGTGGATCAG AATGCCACGG TGAATACGTT	1380

CCCGGGCCTT GTACACACCG CCCGTCACAC CATGGGAGTG GGTGCAAAA GAAGTAGGTA 1440  
 GCTTAACCTT CGGGAGGGCG CTTACCACTT TGTGATTCAT GACTGGGGTG AAGTCGTAAC 1500  
 5 AAGGTAACCG TAGGGGAACC TGCGGTTGGA TCACCTCCTT A 1541

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACAGGAAGA AGCTTGCTCT TTGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AACAGGAAGC AGCTTGCTGT TTCGCTGACG A 31

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACAGGAAAC AGCTTGCTGT TTCGCTGACG A 31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AACAGAAAGC AGCTTGCTCT TTGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 AACAGGAAGC AGCTTGCTCT TCGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGCAACG CGAAGAACCT TACCTGGTCT T 31

20 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30 CGACGCAACG CGAAGAACTT ACCTGGTCTT 30

(2) INFORMATION FOR SEQ ID NO:15:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

45 GGAAGTTTT TC AGAGATGAGA ATGTGCCTTC GGAACCGTG 40

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGAAGTTTCC AGAGATGGAT TGGTGCCTTC GGAAGCTGTG 40

60 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 AGAAGCTTCC AGAGATGGAT TGGTGCCTTC GGGAACTGTG 40

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20 CAGCTTGCTC TTCGCTGACG 20

(2) INFORMATION FOR SEQ ID NO:19:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35 AAAGCAGCTT GCTCTTTGCT 20

(2) INFORMATION FOR SEQ ID NO:20:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

50 CGACGCAACG CGAAGAACTT 20

(2) INFORMATION FOR SEQ ID NO:21:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

65 GAAGCTTGCT TCTTTGCTGA C 21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACGCAACG CGAAGAA

17

09027439 022008